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# 2

## RAW SEQUENCE LISTING

DATE: 07/30/2001

PATENT APPLICATION: US/09/776,696

TIME: 15:52:01

Input Set : N:\Crf3\RULE60\09776696.txt

Output Set: N:\CRF3\07302001\I776696.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Zhou, Shibin  
 6 Zawel, Leigh  
 7 Vogelstein, Bert  
 8 Kinzler, Kenneth

10 (ii) TITLE OF INVENTION: Human Fast-1 Gene

13 (iii) NUMBER OF SEQUENCES: 18

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Banner & Witcoff  
 17 (B) STREET: 1001 G Street, NW  
 18 (C) CITY: Washington  
 19 (D) STATE: DC  
 20 (E) COUNTRY: USA  
 21 (F) ZIP: 20001

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Diskette  
 25 (B) COMPUTER: IBM Compatible  
 26 (C) OPERATING SYSTEM: DOS  
 27 (D) SOFTWARE: FastSEQ for Windows Version 2.0

29 (vi) CURRENT APPLICATION DATA:

C--&gt; 30 (A) APPLICATION NUMBER: US/09/776,696

C--&gt; 31 (B) FILING DATE: 06-Feb-2001

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 09/113,309  
 36 (B) FILING DATE:

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Kagan, Sarah A  
 42 (B) REGISTRATION NUMBER: 32141  
 43 (C) REFERENCE/DOCKET NUMBER: 01107.10898

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: 202-508-9100  
 47 (B) TELEFAX: 202-508-9299  
 48 (C) TELEX:

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 1793 base pairs  
 55 (B) TYPE: nucleic acid  
 56 (C) STRANDEDNESS: single  
 57 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62	GTTGAGTCAA TGTGTCCCCC TCTTGTTCCT AGGGTGCGGG CTTTCATGGCC TTCTCCTCCA	60
63	GGAAGCTCCA CCTGATCATG TCCTGGGTGG ATATCCAGCC CCCATAGTTC AGGGCCTACT	120
64	AGCAGCTGCT AGATCTTGAA CTCCAGGAGC GCCCCACGCC TTGGGAGCTT GGCATGGGCT	180
65	AAATACTCCC CCATTTGTTA AATGGGGTCC TGAAACCTGA CCAGGGAAGA CGGGATAAAG	240
66	TAGCCATGGG TCATCGCAGC CCCTTTGAAG CCGGGCCTGG CCACCCAAAG GCAACTCAGG	300

ENTERED

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```

67 GGTGGAGACT GAGGCCTCAG GAGAAGCCCC CACTAGAATG CTCTCTGCCC CTCCCTTCCA 360
68 GATTAACCAA AACCTGCTAA TTGTGGAAGC CCTCGGCATG CTCCCTCCC CCACAGCCTC 420
69 TTCCTCCCTT CCCTCCCCTC CCCCTTCCAT CCGAATGATA AAGGCCCCAG CCCGCCTGCC 480
70 CCAGCCCCGGC CTCAGGTCCC GGCCTTGCTT TCTACACTGC CCCACCGCCC TGCACCTCC 540
71 ACCCGGCCAG GCCCTGCCC ACGCTGCTA CCGTCCCGCA TGGGGCCCTG CAGCGGCTCC 600
72 CGCCTGGGGC CCCCAGAGGC AGAGTCGCCC TCCAGCCCC CTAAGAGGAG GAAGAAGAGG 660
73 TACCTGCGAC ATGACAAGCC CCCCTACACC TACTTGGCCA TGATCGCCTT GGTGATTGAG 720
74 GCCGCTCCCT CCCGCAGACT GAAGCTGGCC CAGATCATCC GTCAGGTCCA GGCCGTGTTC 780
75 CCCTTCTTCA GGGAAGACTA CGAGGGCTGG AAAGACTCCA TTCGCCACAA CCTTTCCTCC 840
76 AACCGATGCT TCCGCAAGGT GCCCAAGGAC CCTGCAAAGC CCCAGGCCAA GGGCAACTTC 900
77 TGGGCGGTCG ACGTGAGCCT GATCCCAGCT GAGGCGCTCC GGCTGCAGAA CACCGCCCTG 960
78 TGCCGGCGCT GGCAGAACGG AGGTGCGCGT GGAGCCTTCG CCAAGGACCT GGGCCCTAC 1020
79 GTGCTGCACG GCGGCCATA CCGGCCGCC AGTCCCCGC CACCACCCAG TGAGGGCTTC 1080
80 AGCATCAAGT CCCTGCTAGG AGGGTCCGGG GAGGGGGCAC CCTGGCCGGG GCTAGCTCCA 1140
81 CAGAGCAGCC CAGTTCCTGC AGGCACAGGG AACAGTGGGG AGGAGGCGGT GCCCACCCCA 1200
82 CCCCTTCCCT CTTCTGAGAG GCCTCTGTGG CCCCTCTGCC CCCTTCCTGG CCCACGAGA 1260
83 GTGGAGGGGG AGACTGTGCA GGGGGGAGCC ATCGGGCCCT CAACCTCTC CCCAGAGCCT 1320
84 AGGGCCTGGC CTCTCCACTT ACTGCAGGGC ACCGCAGTTC CTGGGGGACG GTCCAGCGGG 1380
85 GGACACAGGG CCTCCCTCTG GGGGCAGCTG CCCACCTCCT ACTTGCCTAT CTACACTCCC 1440
86 AATGTGGTAA TGCCCTTGGC ACCACCACCC ACCTCCTGTC CCCAGTGTCC GTCAACCAGC 1500
87 CCTGCCTACT GGGGGGTGGC CCCTGAAACC CGAGGGCCCC CAGGGCTGCT CTGCGATCTA 1560
88 GACGCCCTCT TCCAAGGGGT GCCACCCAAC AAAAGCATCT ACGACGTTT GGTGAGCCAC 1620
89 CCTCGGGACC TGGCGGCCCT TGGCCAGGC TGGCTGCTCT CCTGGTGCAG CCTGTGAGGC 1680
90 TCTTAAGACA GGGGCCGCTC CTCCCTCCCG CTCCACCCC CACCTTGTTG ACAGGGAGCA 1740
91 AGGGAGGCGG CTGTCTGCGA CACAGCAGCT CGAAAACCAG GCAGAGCTTG TTG 1793

```

93 (2) INFORMATION FOR SEQ ID NO: 2:

95 (i) SEQUENCE CHARACTERISTICS:

96 (A) LENGTH: 365 amino acids

97 (B) TYPE: amino acid

98 (C) STRANDEDNESS: single

99 (D) TOPOLOGY: linear

102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

104 Met Gly Pro Cys Ser Gly Ser Arg Leu Gly Pro Pro Glu Ala Glu Ser
105 1 5 10 15
106 Pro Ser Gln Pro Pro Lys Arg Arg Lys Lys Arg Tyr Leu Arg His Asp
107 20 25 30
108 Lys Pro Pro Tyr Thr Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Ala
109 35 40 45
110 Ala Pro Ser Arg Arg Leu Lys Leu Ala Gln Ile Ile Arg Gln Val Gln
111 50 55 60
112 Ala Val Phe Pro Phe Phe Arg Glu Asp Tyr Glu Gly Trp Lys Asp Ser
113 65 70 75 80
114 Ile Arg His Asn Leu Ser Ser Asn Arg Cys Phe Arg Lys Val Pro Lys
115 85 90 95
116 Asp Pro Ala Lys Pro Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val
117 100 105 110
118 Ser Leu Ile Pro Ala Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys
119 115 120 125
120 Arg Arg Trp Gln Asn Gly Gly Ala Arg Gly Ala Phe Ala Lys Asp Leu

```

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```

121      130      135      140
122 Gly Pro Tyr Val Leu His Gly Arg Pro Tyr Arg Pro Pro Ser Pro Pro
123 145      150      155      160
124 Pro Pro Pro Ser Glu Gly Phe Ser Ile Lys Ser Leu Leu Gly Gly Ser
125      165      170      175
126 Gly Glu Gly Ala Pro Trp Pro Gly Leu Ala Pro Gln Ser Ser Pro Val
127      180      185      190
128 Pro Ala Gly Thr Gly Asn Ser Gly Glu Glu Ala Val Pro Thr Pro Pro
129      195      200      205
130 Leu Pro Ser Ser Glu Arg Pro Leu Trp Pro Leu Cys Pro Leu Pro Gly
131      210      215      220
132 Pro Thr Arg Val Glu Gly Glu Thr Val Gln Gly Gly Ala Ile Gly Pro
133 225      230      235      240
134 Ser Thr Leu Ser Pro Glu Pro Arg Ala Trp Pro Leu His Leu Leu Gln
135      245      250      255
136 Gly Thr Ala Val Pro Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser
137      260      265      270
138 Leu Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn
139      275      280      285
140 Val Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro
141      290      295      300
142 Ser Thr Ser Pro Ala Tyr Trp Gly Val Ala Pro Glu Thr Arg Gly Pro
143 305      310      315      320
144 Pro Gly Leu Leu Cys Asp Leu Asp Ala Leu Phe Gln Gly Val Pro Pro
145      325      330      335
146 Asn Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala
147      340      345      350
148 Ala Pro Gly Pro Gly Trp Leu Leu Ser Trp Cys Ser Leu
149      355      360      365

```

151 (2) INFORMATION FOR SEQ ID NO: 3:

153 (i) SEQUENCE CHARACTERISTICS:

154 (A) LENGTH: 477 amino acids

155 (B) TYPE: amino acid

156 (C) STRANDEDNESS: single

157 (D) TOPOLOGY: linear

160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

162 Val Ala Met Ile Asn Ala Cys Ile Asp Ser Met Ser Ser Ile Leu Pro
163 1      5      10      15
164 Phe Thr Pro Pro Val Val Lys Arg Leu Gly Trp Lys Lys Ser Ala
165      20      25      30
166 Gly Gly Ser Gly Gly Ala Gly Gly Glu Gln Asn Gly Gln Glu Glu
167      35      40      45
168 Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys
169      50      55      60
170 Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Cys
171      65      70      75      80
172 Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile Trp Gly
173      85      90      95
174 Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly Leu Tyr

```

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```

175      100      105      110
176 Ser Phe Ser Glu Gln Thr Arg Ser Leu Asp Gly Arg Leu Gln Val Ser
177      115      120      125
178 His Arg Lys Gly Leu Pro His Val Ile Tyr Cys Arg Leu Trp Arg Trp
179      130      135      140
180 Pro Asp Leu His Ser His Glu Leu Lys Ala Ile Glu Asn Cys Glu
181      145      150      155      160
182 Tyr Ala Phe Asn Leu Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His
183      165      170      175
184 Tyr Gln Arg Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg
185      180      185      190
186 His Thr Glu Ile Leu Thr Glu Leu Pro Pro Leu Asp Asp Tyr Thr His
187      195      200      205
188 Ser Ile Pro Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser
189      210      215      220
190 Asn Tyr Ile Pro Glu Thr Pro Pro Pro Gly Tyr Ile Ser Glu Asp Gly
191      225      230      235      240
192 Glu Thr Ser Asp Gln Gln Leu Asn Gln Ser Met Asp Thr Gly Ser Pro
193      245      250      255
194 Ala Glu Leu Ser Pro Thr Thr Leu Ser Pro Val Asn His Ser Leu Asp
195      260      265      270
196 Leu Gln Pro Val Thr Tyr Ser Glu Pro Ala Phe Trp Cys Ser Ile Ala
197      275      280      285
198 Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln
199      290      295      300
200 Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg
201      305      310      315      320
202 Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg Asn Ala Thr Val Glu
203      325      330      335
204 Met Thr Arg Arg His Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly
205      340      345      350
206 Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln
207      355      360      365
208 Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys
209      370      375      380
210 Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe
211      385      390      395      400
212 Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr
213      405      410      415
214 Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp
215      420      425      430
216 Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile
217      435      440      445
218 Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr
219      450      455      460
220 Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser
221      465      470      475
223 (2) INFORMATION FOR SEQ ID NO: 4:
225      (i) SEQUENCE CHARACTERISTICS:

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/776,696

DATE: 07/30/2001

TIME: 15:52:02

Input Set : N:\Crf3\RULE60\09776696.txt

Output Set: N:\CRF3\07302001\I776696.raw

```

226      (A) LENGTH: 8 base pairs
227      (B) TYPE: nucleic acid
228      (C) STRANDEDNESS: single
229      (D) TOPOLOGY: linear
232      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
234      TGTKKATT 8
236      (2) INFORMATION FOR SEQ ID NO: 5:
238      (i) SEQUENCE CHARACTERISTICS:
239      (A) LENGTH: 18 base pairs
240      (B) TYPE: nucleic acid
241      (C) STRANDEDNESS: single
242      (D) TOPOLOGY: linear
245      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
247      CTGGAAAGAC TCCATTCG 18
249      (2) INFORMATION FOR SEQ ID NO: 6:
251      (i) SEQUENCE CHARACTERISTICS:
252      (A) LENGTH: 19 base pairs
253      (B) TYPE: nucleic acid
254      (C) STRANDEDNESS: single
255      (D) TOPOLOGY: linear
258      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
260      CACAGAGGCC TCTCAGAAG 19
262      (2) INFORMATION FOR SEQ ID NO: 7:
264      (i) SEQUENCE CHARACTERISTICS:
265      (A) LENGTH: 18 base pairs
266      (B) TYPE: nucleic acid
267      (C) STRANDEDNESS: single
268      (D) TOPOLOGY: linear
271      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
273      CCCCTTCCA TCCGAATG 18
275      (2) INFORMATION FOR SEQ ID NO: 8:
277      (i) SEQUENCE CHARACTERISTICS:
278      (A) LENGTH: 19 base pairs
279      (B) TYPE: nucleic acid
280      (C) STRANDEDNESS: single
281      (D) TOPOLOGY: linear
284      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
286      GAGCTGCTGT GTCGCAGAC 19
288      (2) INFORMATION FOR SEQ ID NO: 9:
290      (i) SEQUENCE CHARACTERISTICS:
291      (A) LENGTH: 79 base pairs
292      (B) TYPE: nucleic acid
293      (C) STRANDEDNESS: single
294      (D) TOPOLOGY: linear
297      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
299      GGATCCTAAT ACGACTCACT ATAGGGAGAC CACCATGGAC TACAAGGACG ACGATGACAA 60
300      GGGGCCCTGC AGCGGCTCC 79
302      (2) INFORMATION FOR SEQ ID NO: 10:
304      (i) SEQUENCE CHARACTERISTICS:

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/776,696

DATE: 07/30/2001

TIME: 15:52:03

Input Set : N:\Crf3\RULE60\09776696.txt

Output Set: N:\CRF3\07302001\I776696.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]